## Expression patterns of a novel *AtCHX* gene family highlight potential roles in osmotic adjustment and K<sup>+</sup> homeostasis in pollen development

Heven Sze, Senthilkumar Padmanaban, Kevin W. Bock & Xiyan Li, University of Maryland, College Park, MD 20742-5815, USA Françoise Cellier&Genevieve Conéjéro, INRA/CNRS/AgroM/UMII, Montpellier, France David Honys, Institute of Experimental Botany AS CR, Praha, Czech Republic Ning-Hui Cheng & Kendal D. Hirschi, Baylor College of Medicine, Houston, TX, USA David Twell, University of Leicester, Leicester LE1 7RH, England John M. Ward, University of Minnesota, St. Paul, MN, USA

A combined bioinformatic and experimental approach is being used to uncover the functions of a novel family of CHX (cation/ $\underline{H}^+$  exchanger) genes in plants using Arabidopsis thaliana as a model. The predicted protein (85-95 kDa) of 28 AtCHX genes after revision consists of an amino-terminal domain with 10-12 transmembrane spans (~440 residues), and a hydrophilic domain of ~360 residues at the carboxyl end which is proposed to have regulatory roles. The hydrophobic, but not the hydrophilic, domain of plant CHX is remarkably similar to monovalent cation/proton antiporter-2 (CPA2) proteins, especially yeast KHA1 and Synechocystis NhaS4. Reports of characterized fungal and prokaryotic CPA2 indicate they have various transport modes, including  $K^+/H^+$  (KHA1),  $Na^+/H^+-K^+$  (GerN) antiport, and ligand-gated ion channel (KefC). The expression pattern of AtCHX genes was determined by reverse-transcription polymerasechain-reaction, promoter-driven GUS expression in transgenic plants, -and Affymetrix ATH1 Genome Arrays. Results show that 18 genes are specifically or preferentially expressed in the male gametophyte and 6 genes are highly expressed in sporophytic tissues. Microarray data revealed that several AtCHX genes were developmentallyregulated during microgametogenesis. An exciting idea is that CHX proteins allow osmotic adjustment and K<sup>+</sup> homeostasis as mature pollen dessicates and then rehydrates at germination. The multiplicity of CHX-like genes is conserved in higher plants, but is not found in animals. Only seventeen genes, OsCHX01-OsCHX17, were identified in Oryza sativa ssp. japonica, suggesting further diversification in Arabidopsis. results reveal a novel CHX gene family in flowering plants with potential functions in pollen development, germination, and tube growth.